

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	AAR27369 TRFP Chai
Run on: October 18, 2005, 13:28:04 ; Search time 166 seconds	(without alignments)	AAY51470 Human TRF
Perfect score: 27	62.907 Million cell updates/sec	AAB28933 T cell re
Title: US-09-662-784-6_COPY_33_59	sequence: 1 FFAVANGNELLIDLSITKVRATEPERT 27	AAY90103 Cat TRFP
Scoring table: OLIIGO	Gapop 60.0 , Gapext 60.0	AAY87673 Feline hu
Searched: 2105692 seqs, 386760361 residues	Word size : 0	AAR1977 Human T C
Total number of hits satisfying chosen parameters: 2105692	Minimum DB seq length: 0	AAR36544 Peptide Z
Maximum DB seq length: 2000000000	Post-processing: listing first 45 summaries	AAY51481 Human TRF
Database : A_Geneseq16Dec04;*	1: Geneseq16Dec04;*	AAB88943 Peptide Z
2: geneseqp1990s;*	2: geneseqp1980s;*	AAY90109 Cat TRFP
3: geneseqp2000s;*	3: geneseqp2001s;*	AAY87684 Feline hu
4: geneseqp2002s;*	4: geneseqp2003as;*	AAR36548 Recombito
5: geneseqp2003bs;*	5: geneseqp2004as;*	AAB28979 Peptide Y
6: geneseqp2003bs;*	6: geneseqp2004as;*	AAY90145 TRFP fusi
7: geneseqp2004as;*	7: geneseqp2004as;*	AAY51478 Human TRF
8: geneseqp2004as;*	8: geneseqp2004as;*	AAB28940 T cell re
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	RESULTS	AAY90106 Cat TRFP
	SUMMARIES	AAY87681 Feline hu
		AAR27372 TRFP Chai
		AAY51487 Human TRF
		ALIGNMENTS
		RESULT 1
Result No.	Score	Query Match Length DB ID Description
1	27	100.0 90 3 AAY51476 Aay51476 Human TRF
2	27	100.0 90 3 AAB28938 Aab28938 T cell re
3	27	100.0 90 3 AAY87679 Aay87679 Feline hu
4	27	100.0 92 3 AAY51475 Human TRF
5	27	100.0 92 3 AAB28937 T cell re
6	27	100.0 92 3 AAY87678 Aay87678 Feline hu
7	27	100.0 97 2 AAR12123 Aar12123 TRFP Chai
8	27	100.0 97 3 AAY51472 Human TRF
9	27	100.0 97 3 AAB28935 T cell re
10	27	100.0 97 3 AAY90105 Cat TRFP
11	27	100.0 97 3 AAY87675 Feline hu
12	27	100.0 10 8 ADO38397 Ado38397 Cat aller
13	27	100.0 107 7 ADR62496 Adr62496 Cat aller
14	27	100.0 109 2 AAR12122 Aar12122 TRFP I ch
15	27	100.0 109 2 AAR41985 Human T C
16	27	100.0 109 2 AAR36541 TRFP chai
17	27	100.0 109 2 AAY25593 Felis sp.
18	27	100.0 109 3 AAY51471 Aay51471 Human TRF
19	27	100.0 109 3 AAB28934 Aab28934 T cell re
20	27	100.0 109 3 AAY90104 Cat TRFP
21	27	100.0 109 3 AAY87674 Feline hu
22	27	100.0 109 7 ADC34843 Cat aller
23	27	100.0 109 8 ADM12179 Cat aller
24	27	100.0 110 2 AAR27370 Aar27370 TRFP Chai
25	100.0 111 2 AAR12121 Aar12121 TRFP chai	Peptides of human T cell reactive feline protein for treating sensitivity to cat protein allergens comprise at least one T cell epitope recognized by a T cell receptor specific for the human T cell reactive feline protein.
		Example 1; Col 83-84; 105pp; English.
		This invention describes a novel peptide (1) of human T cell reactive feline protein (hTRFP) having at least one T cell epitope recognized by a T cell receptor specific for the human T cell reactive feline protein, the peptide consisting of at least 7-10 amino acids, and having an amino acid sequence derived from an amino acid sequence comprising 94, 96, 97,

109, or 111 residues, given in the specification. The peptides down
regulate the immune response to the allergen. The peptides have reduced
immunoglobulin E binding and reduce T cell responsiveness. The peptide
(I) is useful in compositions for treating sensitivity to a cat protein
allergen in a subject. This sequence represents the human TRPP chain 2
(short form)

XX SQ Sequence 90 AA;

Query Match 100.0%; Score 27; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.9e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDSLTKVNAPEPERT 27
ID 14 FFAVANGNELLIDSLTKVNAPEPERT 40
Db

RESULT 2
AAB28938
ID AAB28938 standard; protein; 90 AA.
XX
AC AAB28938;
XX
DT 29-JAN-2001 (first entry)
DB T cell reactive feline protein chain 2 PRO short.
XX
Cat; allergy; human T cell reactive feline protein; hTRPP; immunotherapy.
XX
OS Felis sp.
XX
PR 03-NOV-1999; 89US-00431565.
PR 28-FEB-1991; 91US-00622276.
PR 13-DEC-1991; 91US-00807529.
PR 25-MAR-1992; 92US-00857311.
PR 15-MAY-1992; 92US-00884718.
PR 15-MAY-1992; 92US-00884718.
PR 15-JAN-1993; 93US-00006116.
PR 02-SEP-1994; 94US-00300928.
XX
PP (IMMU-) IMMULOGIC PHARM CORP.
XX
PR 03-NOV-1989; 89US-00431565.
PR 28-FEB-1991; 91US-00622276.
PR 13-DEC-1991; 91US-00807529.
PR 25-MAR-1992; 92US-00857311.
PR 15-MAY-1992; 92US-00884718.
PR 02-SEP-1994; 94US-00300928.
XX
PT Geffter ML, Garman RD, Greenstein JL, Bond JP;
DR WPI; 2000-601477/57.

PT Detecting, preventing and treating sensitivity to cat protein allergen
PT comprises combining a biological sample with a human T cell reactive
PT feline protein and determining the extent of binding that occurs.

PS Disclosure; Fig 7; 106pp; English.

CC The present invention relates to the detection of sensitivity to a cat
protein allergen by combining a blood sample from a subject with a cat
peptide of human T cell reactive feline protein (hTRPP). This method and
CC the hTRPP peptides are useful for diagnosing, preventing and treating cat
allergies by reducing or abolishing an individual's allergic response to
a cat allergen. DNA encoding the TRPP may be used as probes to locate
CC equivalent sequences present in other species. These may further be used
to study the mechanism of immunotherapy of cat allergy, and to design
CC modified derivatives, analogues or functional equivalents useful in
CC immunotherapy. The present sequence was used in the invention

XX SQ Sequence 90 AA;

Query Match 100.0%; Score 27; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.9e-19;

	Matches	27; Conservative 0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	FFAVANGNELLIDSLTKVNAPEPERT	27					
Db	14	FFAVANGNELLIDSLTKVNAPEPERT	40					

RESULT 3
AY87679

ID AAY87679 standard; protein; 90 AA.

XX AAY87679;

XX DR Feline human TRPP chain 2 short form protein #2.

XX KW T-cell reactive feline protein; TRPP; Fel d I; cat allergen;
antiallergic; T cell stimulator; diagnostic; immunotherapy.

XX OS Felis sp.

XX PN US6048962-A.

XX PD 11-APR-2000.

XX PF 27-APR-1995; 95US-00430014.

XX PR 03-NOV-1999; 89US-00431565.

PR 28-FEB-1991; 91US-00622276.

PR 13-DEC-1991; 91US-00807529.

PR 25-MAR-1992; 92US-00857311.

PR 15-MAY-1992; 92US-00884718.

PR 15-JAN-1993; 93US-00006116.

PR 02-SEP-1994; 94US-00300928.

XX PA (IMMU-) IMMULOGIC PHARM CORP.

XX PI Kuo M, Rogers BL, Geffter ML, Morgenstern JP, Brauer AW;

XX DI Greenstein JL, Griffith JF, Garman RD;

XX DR WPI; 2000-316905/27.

XX Example 2; Col 83-84; 106pp; English.

CC This invention describes a novel naturally occurring cat protein allergen
(I), human T cell reactive feline protein (TRPP), comprising two
CC different covalently linked peptide chains with a molecular weight of 20
KD, 40 KD or 130 KD under non-reducing conditions and 5 KD or 10-18 KD
CC under reducing conditions. The products of the invention have
antiallergic activity and act as human T cell stimulators. TRPP is useful
CC for reducing or preventing the adverse effects of cat allergens on cat
allergic individuals and in ex vivo diagnostic tests to determine which
CC peptides cause sensitivity so as to selectively use them to desensitize a
CC sensitive individual. Purified TRPP is also useful for studying the
CC mechanism of immunotherapy of cat allergy and to design modified
CC derivatives, analogs or functional equivalents that are more useful in
CC immunotherapy against cat allergy. DNA sequences encoding TRPP are useful
CC as probes to locate equivalent sequences present in other species (goats,
CC sheep, dogs, rabbits or horses) that may be useful in diagnostics and/or
CC therapeutics. Fully defined and characterized TRPP provides complete and
CC a very simple desensitization therapy. This sequence represents a human T
CC cell reactive feline protein (also known as Fel d I) chain 2, short form
CC which is described in the method of the invention

XX SQ Sequence 90 AA;

Query Match 100.0%; Score 27; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.9e-19;

KW antiallergic; T cell stimulator; diagnostic; immunotherapy.
XX
OS Felis sp.
XX
PN US6048962-A.
XX
PD 11-APR-2000.
XX
PF 27-APR-1995; 95US-00430014.
XX
PR 03-NOV-1989; 89US-00431565.
PR 28-FEB-1991; 91US-00662376.
PR 13-DEC-1991; 91US-00807529.
PR 25-MAR-1992; 92US-00857311.
PR 15-MAY-1992; 92US-00884718.
PR 15-JAN-1993; 93US-00006116.
PR 02-SEP-1994; 94US-00300928.
XX
PA (IMMU-) IMMULOGIC PHARM CORP.
XX
PT Kuo M, Rogers BL, Gefter ML, Morgenstern JP, Brauer AW;
PI Greenstein JL, Griffith IJ, Garman RD;
XX
DR WPI; 2000-316905/27.
XX
PT New human T cell reactive feline protein useful for reducing or
PT abolishing individual's allergic response to cat allergen comprising two
PT different covalently linked peptide chains.
XX
PS Example 2; Col 81-84; 106pp; English.
XX
CC This invention describes a novel naturally occurring cat protein allergen
CC (1), human T cell reactive feline protein (TRFP), comprising two of 20
CC different covalently linked peptide chains with a molecular weight of 20
CC kd, 40 kd or 130 kd under non-reducing conditions and 5 kd or 10-18 kd
CC under reducing conditions. The products of the invention have
CC antiallergic activity and act as human T cell stimulators. TRFP is useful
CC for reducing or preventing the adverse effects of cat allergens on cat
CC allergic individuals and in ex vivo diagnostic tests to determine which
CC peptides cause sensitivity so as to selectively use them to desensitize a
CC cat sensitive individual. Purified TRFP is also useful for studying the
CC mechanism of immunotherapy of cat allergy and to design modified
CC derivatives, analogs or functional equivalents that are more useful in
CC immunotherapy against cat allergy. DNA sequences encoding TRFP are useful
CC as probes to locate equivalent sequences present in other species (goats,
CC sheep, dogs, rabbits or horses) that may be useful in diagnostics and/or
CC therapeutic. Fully defined and characterized TRFP provides complete and
CC a very simple desensitization therapy. This sequence represents a human T
CC cell reactive feline protein (also known as Fel d 1) chain 2, long form
CC which is described in the method of the invention
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 27; DB 3; Length 92;
 Best Local Similarity 100.0%; Pred. No. 3e-19; Mismatches 0; Indels 0; Gaps 0;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDLSDLSITKVNATEPERT 27
 Db 14 FFAVANGNELLIDLSDLSITKVNATEPERT 40

RESULT 7
 AAR12123
 ID AAR12123 standard; protein; 97 AA.
 XX
 AC AAR12123;
 AC AAR12123;
 DT 26-JUL-1991 (first entry)
 DB TRFP chain 2 - truncated short form.
 XX
 KW Human T cell reactive feline protein; cat allergens.

XX
 OS Felis catus.
 XX
 PR Key peptide 3..19
 FT /label= Leader sequence
 FT 20..97 /label= TRFP 1 truncated short form
 FT
 FT WO9106571-A.
 XX
 PR 16-MAY-1991.
 XX
 PR 03-NOV-1989; 89US-00431565.
 XX
 PR 03-NOV-1989; 89US-00431565.
 XX
 PR (IMMU-) IMMULOGIC PHARM COR.
 XX
 PT Gefter ML, Garman RD, Greenstein JL, Juo M, Rogers BL, Brauer AW;
 XX
 DR WPI; 1991-164136/22.
 DR N-PSDB; A9Q11840.
 XX
 PR New pure covalently linked human T cell reactive feline protein - and
 PR modified peptide(s), used to reduce effects of cat allergens and to
 PR diagnose sensitivity to allergens.
 XX
 PS Claim 2; Fig 5; 70pp; English.
 XX
 CC POLY-A mRNA from cat parotid and mandibular glands was used to produce
 CC cDNA clones for both chain 1 and chain 2 of TRFP. These clones were then
 CC used to screen a cat genomic library. Chain 1 exists in two forms having
 CC different protein leader sequences (A and B). The sequence can be used to express
 CC the protein and peptide derive, which stimulate T-cells in persons
 CC allergic to cats. The peptides can be used to reduce/eliminate the
 CC allergic response partic. by modifn. of lymphokine prodn. by the T-
 CC cells. They can also be used to identify epitopes responsible for
 CC sensitivity. The DNA can be used to detect comparable sequence in other
 CC species, and also for prodn. of modified forms of TRFP esp. showing
 CC reduced binding to IgE and thus reduced tendency to cause adverse
 CC reactions. See also AAR1219-R12122
 XX
 SQ Sequence 97 AA;

Query Match 100.0%; Score 27; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 3.1e-19; Mismatches 0; Indels 0; Gaps 0;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDLSDLSITKVNATEPERT 27
 Db 33 FFAVANGNELLIDLSDLSITKVNATEPERT 59

RESULT 8
 AAY51472
 ID AAY51472 standard; protein; 97 AA.
 XX
 AC AAY51472;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Human TRFP chain 2 (truncated form) protein fragment.
 XX
 T-cell reactive feline protein; TRFP; T cell epitope; T cell receptor;
 KW down regulation; immune response; allergen; immunoglobulin E;
 KW sensitivity; cat protein allergen; human; chain 2.
 XX
 OS Homo sapiens.
 PN US6019972-A.
 XX
 PD 01-FEB-2000.

PR	02-SEP-1994;	94US-00300928.
XX		
PR	03-NOV-1989;	89US-00431565.
PR	28-FEB-1991;	91US-00622276.
PR	13-DEC-1991;	91US-00807529.
PR	25-MAR-1992;	92US-00857311.
PR	15-MAY-1992;	92US-00884718.
PR	15-JAN-1993;	93US-0006116.
PR		
XX		
PA	(IMMU-) IMMULOGIC PHARM CORP.	
XX		
PT	Gaftor ML, Garman RD, Greenstein JL, Bond JP;	
XX		
DR	WPI; 2000-501477/57.	
DR	N-PSDB; AAC60105.	
XX		
XX	Detecting, preventing and treating sensitivity to cat protein allergen	
PT	comprises combining a biological sample with a human T cell reactive	
PT	cat protein and determining the extent of binding that occurs.	
XX		
PS	Claim 1; Fig 5; 106pp; English.	
XX		
XX	This invention describes a novel peptide (I) of human T cell reactive	
CC	cat feline protein (hTRPP) having at least one T cell epitope recognized by a	
CC	T cell receptor specific for the human T cell reactive feline protein, hTRPP. This method and	
CC	peptide of human T cell reactive feline protein (hTRPP). This method and	
CC	the hTRPP peptides are useful for diagnosing, preventing and treating cat	
CC	allergies by reducing or abolishing an individual's allergic response to	
CC	a cat allergen. DNA encoding the TRPP may be used as probes to locate	
CC	equivalent sequences present in other species. These may further be used	
CC	to study the mechanism of immunotherapy of cat allergy, and to design	
CC	modified derivatives, analogues or functional equivalents useful in	
CC	immunotherapy. The present sequence was used in the invention.	
XX		
SQ	Sequence 97 AA;	
XX		
Query	Match	100.0%; Score 27; DB 3; Length 97;
Best	Local	Similarity
Matches	27;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QV	1	FFAVANGNELLDDLSLTKVNATEPERT 27
CC		
Db	33	FFAVANGNELLDDLSLTKVNATEPERT 59
CC		
XX		
RESULT	9	
AAB28935		
ID	AB28935	standard; protein; 97 AA.
XX		
AC	AAB28935;	
XX		
DT	29-JAN-2001	(first entry)
XX		
DE	T cell reactive feline protein chain 2 truncated form.	
XX		
KW	Cat; allergy; human T cell reactive feline protein; hTRPP; immunotherapy.	
XX		
OS	Felis sp.	
XX		
PN	US6120769-A.	
XX		
PD	19-SEP-2000.	
XX		
PF	28-APR-1995;	95US-00431184.
XX		
PF	03-NOV-1989;	89US-00431565.
PR	28-FEB-1991;	91US-00622276.
PR	13-DEC-1991;	91US-00807529.
PR	25-MAR-1992;	92US-00857311.
PR	15-MAY-1992;	92US-00884718.
PR	15-JAN-1993;	93US-0006116.
PR		
XX		
XX	RESULT	10
XX	Sequence	97 AA;
XX		
Query	Match	100.0%; Score 27; DB 3; Length 97;
Best	Local	Similarity
Matches	27;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QV	1	FFAVANGNELLDDLSLTKVNATEPERT 27
Db	33	FFAVANGNELLDDLSLTKVNATEPERT 59
XX		
RESULT	10	
XX		
AY90105		
ID	AY90105	standard; protein; 97 AA.
XX		
AC	AY90105;	
XX		
DT	12-SEP-2003	(revised)
DT	13-JUN-2000	(first entry)
XX		
DB	Cat TRPP chain 2 truncated form protein sequence.	
XX		
Cat	TRPP; human T-cell reactive feline protein; cat protein allergen;	
KW	house dust; Fel d 1; cat allergy; Felis domesticus sensitivity; therapy;	
KW	diagnosis; goat; sheep; horse; rabbit; dog.	
XX		
OS	Felis catus.	
XX		
FR	Key	location/qualifiers
FT	Peptide	1..19
FT		/note= "signal peptide"
FT	Protein	20..97
FT		note= "mature TRPP chain 2 truncated form"
XX		
PN	US6025162-A.	
XX		
PD	15-FEB-2000.	
XX		
PF	28-APR-1995;	95US-00430944.
XX		
PR	03-NOV-1989;	89US-00431565.
PR	28-FEB-1991;	91US-00622276.
PR	13-DEC-1991;	91US-00807529.
PR	25-MAR-1992;	92US-00857311.
PR	15-MAY-1992;	92US-00884718.
PR	15-JAN-1993;	93US-0006116.
PR		

PA	(ANTI-) ANTIGEN EXPRESS INC.	OS	Felis catus.
XX		XX	
PI	Humphreys RE, Xu M;	Key	Location/Qualifiers
XX		FH	
DR	WPI; 2004-294259/27.	PT	1..17
XX		FT	/label= Leader_peptide
PT	New non-naturally occurring protein or polypeptide modified by recombinant DNA techniques, useful for treating multiple sclerosis, diabetes mellitus, myasthenia gravis, scleroderma, allergic rhinitis, colitis, cancer or psoriasis.	FT _x	18..107
XX		FT _x	/note= "Nature Fel d 1 chain 2 protein"
PT		XX	US2003177512-A1.
PT		PN	
PT		XX	18-SEP-2003.
XX		PD	
PS	Example 4; Page 24; 90pp; English.	XX	
CC	The invention relates to a non-naturally occurring protein or polypeptide (1) modified by recombinant DNA techniques comprising: a C-terminal element comprising an MHC Class II-presented epitope; an N-terminal element comprising an Ii-key motif; and an intervening element comprising a sequence of 4-11 amino acid residues where the modification by recombinant DNA techniques taking place within elements (b) and (c). Also described are methods for: suppressing or enhancing an immune response directed toward an MHC (major histocompatibility complex) Class II-presented epitope of interest. Suppressing an immune response directed toward an MHC Class II-presented epitope of interest comprises: providing a nucleic acid sequence encoding the MHC Class II-presented epitope of interest, the nucleic acid sequence encoding an Ii-Key motif located 4-11 amino acids upstream from the N-terminal residue of the MHC Class II-presented epitope of interest; and modifying its conformation to the archetypal Ii-key regulatory motif. Enhancing an immune response directed toward an MHC Class II-presented epitope of interest comprises: providing a nucleic acid sequence encoding the MHC Class II-presented epitope of interest, the nucleic acid sequence lacking an Ii-key motif located 4-11 amino acids upstream from the N-terminal residue of the MHC Class II-presented epitope of interest; and modifying the nucleic acid sequence to introduce an Ii-key motif appropriately spaced from the MHC Class II-presented epitope. The protein or polypeptide of interest corresponds to a protein or polypeptide encoded by an infectious pathogen selected from anthrax, Ebola, HIV or influenza, preferably vaccinia virus. The non-naturally occurring protein or polypeptide (1) modified by recombinant DNA techniques is useful for treating infectious diseases caused or associated with infection by a bacterium, virus, parasite, fungus, rickettsia or other infectious agents. It is also useful for treating rheumatoid arthritis, multiple sclerosis, lupus erythematosus, diabetes mellitus, myasthenia gravis, autoimmune thyroiditis, scleroderma, dermatomyositis, pemphigus, asthma, allergic rhinitis, topical dermatitis, colitis, cancer, psoriasis or adenomas. The present sequence represents the amino acid sequence of a cat allergen Fel d1 chain 1 MHC class II-presented epitope used in the invention.	XX	
XX	Sequence 100 AA;	XX	
Query Match	100.0%; Score 27; DB 8; Length 100; Best Local Similarity 100.0%; Pred. No. 3.2e-19; Mismatches 27; Conservative 0; Indels 0; Gaps 0;	XX	
Matches	27; Conservative 0; Indels 0; Gaps 0;	Key	Location/Qualifiers
Qy	1 FRAVANGNELLIDSLTKVATEPERT 27	FH	
Db	31 FRAVANGNELLIDSLTKVATEPERT 57	PT	1..17
RESULT 13		FT	/label= Leader_peptide
ADH62496		FT _x	18..107
ID	ADH62496 standard; protein; 107 AA.	FT _x	/note= "Nature Fel d 1 chain 2 protein"
XX		XX	US2003177512-A1.
AC	ADH62496;	PN	
XX		XX	18-SEP-2003.
DT	25-MAR-2004 (first entry)	PD	
XX		XX	
DE	Cat allergen Fel d 1 (chain 2) protein.	XX	
XX	Allergen; vaccine; gene therapy; transgenic animal; Fel d 1; embryonic stem cell; allergy; cat.	XX	
KW		DE	TRFP 1 chain 2 - short form.
XX		XX	
Query Match	100.0%; Score 27; DB 7; Length 107; Best Local Similarity 100.0%; Pred. No. 3.4e-19; Mismatches 27; Conservative 0; Indels 0; Gaps 0;	OS	Felis catus.
Matches	27; Conservative 0; Indels 0; Gaps 0;	XX	
Qy	1 FRAVANGNELLIDSLTKVATEPERT 27	Key	Location/Qualifiers
Db	31 FRAVANGNELLIDSLTKVATEPERT 57	FH	
RESULT 14		PT	1..17
ADH62496		FT	/label= Leader_peptide
ID	ADH62496 standard; protein; 109 AA.	FT _x	18..107
XX		FT _x	/note= "Nature Fel d 1 chain 2 protein"
AC	ADH62496;	XX	US2003177512-A1.
XX		PN	
DT	26-JUL-1991 (first entry)	XX	18-SEP-2003.
XX		PD	
DE	TRFP 1 chain 2 - short form.	XX	
XX		XX	

KW Human T cell reactive feline protein; cat allergens.
 XX
 OS *Felis catus*.
 XX
 FH Key Peptide
 FT Location/Qualifiers
 FT 3..19
 FT /label= Header sequence
 FT 20..111
 FT /label= TRFP I short form
 XX
 PN WO9106571-A.
 XX
 PD 16-MAY-1991.
 XX
 PR 03-NOV-1989; 89US-00431565.
 XX
 PR 03-NOV-1989; 89US-00431565.
 XX
 PA (IMMU-) IMMUNOLOGIC PHARM COR.
 XX
 PI Gefter ML, Garman RD, Greenstein JL, Juo M, Rogers BL, Brauer AW,
 XX
 DR WPI; 1991-164135/22.
 DR N-PSDB; AAQ1839.
 XX
 PT New pure covalently linked human T cell reactive feline protein - and
 PT modified peptide(s), used to reduce effects of cat allergens and to
 PT diagnose sensitivity to allergens.
 XX
 PS Claim 2; FIG 4; 70pp; English.
 XX
 CC POLY-A mRNA from cat parotid and mandibular glands was used to produce
 CC cDNA clones for both chain 1 and chain 2 of TRFP. These clones were then
 CC used to screen a cat genomic library. Chain 1 exists in two forms having
 CC different leader sequences (A and B). The sequence can be used to express
 CC the protein and peptide derive which stimulate T cells in persons
 CC allergic to cats. The peptides can be used to reduce/eliminate the
 CC allergic response partic. by modifn. of lymphokine prodn. by the T-
 CC cells. They can also be used to identify epitopes responsible for
 CC sensitivity. The DNA can be used to detect comparable sequence in other
 CC species, and also for prodn. of modified forms of TRFP esp. showing
 CC reduced binding to IgE and thus reduced tendency to cause adverse
 CC reactions. See also AAR12119-R12123
 SQ Sequence 109 AA;

Query Match 100.0%; Score 27; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 3.5e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDSLTSITKVNATEPERT 27
 Db 33 FFAVANGNELLIDSLTSITKVNATEPERT 59

RESULT 15

AAR4185
 ID AAR41985 standard; protein: 109 AA.
 XX
 AC AAR4185;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-APR-1994 (first entry)
 DE Human T cell reactive feline protein chain 2.
 XX
 KW Human; T cell; reactive; feline; protein; immune response; antigen;
 KW tolerance; mammal; Dermatophagoides; *Felis*; *Ambrosia*; *Lolium*; *Canis*;
 KW *Cryptomeria*; *Alternaria*; *Alder*; *Betula*; *Quercus*; *Olea*; *Artemesia*;
 KW *Plantago*; *Parietaria*; *Blattella*; *Apis*; *Periplaneta*; autoantigen.
 OS Homo sapiens.
 XX

FH Key Peptide
 FT Location/Qualifiers
 FT 1..17
 FT /note= "Signal peptide"
 FT 18..109
 FT /note= "Mature protein"
 XX
 PN WO9319178-A2.
 XX
 PD 30-SEP-1993.
 XX
 PR 25-MAR-1993; 93WO-US002462.
 XX
 PR 25-MAR-1992; 92US-00857311.
 PR 15-MAY-1992; 92US-00884718.
 PR 15-JAN-1993; 93US-00006116.
 XX
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX
 PI Gefter ML, Garman RD, Greenstein JL, Kuo M, Briner TJ;
 PI Morville M;
 XX
 DR WPI; 1993-320744/40.
 DR N-PSDB; AAQ4935.
 XX
 PT New peptide(s) for inducing tolerance - comprise one or more epitope(s)
 PT of an allergen administered subcutaneously, for treating sensitivity to
 PT cats, bees, etc.
 XX
 PS Disclosure; Fig 2; 107pp; English.
 XX
 CC This sequence represents chain 2 of human T cell reactive feline protein
 CC (TRFP). Peptides derived from TRFP may be used in a therapeutic
 CC composition which is useful in treating disease which involve an immune
 CC response to a protein antigen. This composition may be used to induce
 CC tolerance in a mammal to Dermatophagoides, *Felis*, *Ambrosia*, *Lolium*,
 CC *Cryptomeria*, *Alternaria*, *Alder*, *Betula*, *Quercus*, *Olea*, *Artemesia*,
 CC *Plantago*, *Parietaria*, *Canis*, *Blattella*, *Apis*, *Periplaneta* and to
 CC autoantigens in humans. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 109 AA;

Query Match 100.0%; Score 27; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 3.5e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDSLTSITKVNATEPERT 27
 Db 31 FFAVANGNELLIDSLTSITKVNATEPERT 57

Search completed: October 18, 2005, 13:44:17
 Job time : 167 Secs

GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on: October 18, 2005, 13:47:36 ; Search time 170 Seconds

Sequence: 1 FPAVANGNELLIDDISKRVNATEBERT 27

Perfect score: 27 US-09-662-784-6_COPY_33_59

Sequence: 1 OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 186064 seqs, 416830855 residues

Word size : 0

Total number of hits satisfying chosen parameters: 186064

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : Published_Applications_AA:*

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3: /cgn2_6/ptodata/2/pupbaa/US06_NEW_PUB.pep:*

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8: /cgn2_6/ptodata/2/pupbaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pupbaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pupbaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pupbaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pupbaa/US09_NEW_PUB.pep:*

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21: /cgn2_6/ptodata/2/pupbaa/US16_NEW_PUB.pep:*

22: /cgn2_6/ptodata/2/pupbaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	27	100.0	107 14 US-10-295-903-4	Sequence 4, Appli
2	27	100.0	109 8 US-08-464-363-6	Sequence 6, Appli
3	27	100.0	109 10 US-09-847-208-98	Sequence 98, Appli
4	27	100.0	109 15 US-10-245-871-136	Sequence 136, Appli
5	27	100.0	109 15 US-10-453-113-6	Sequence 6, Appli
6	27	100.0	109 15 US-10-253-206-136	Sequence 136, Appli
7	27	100.0	109 16 US-10-809-639-32	Sequence 32, Appli
8	26	96.3	8 US-08-464-363-9	Sequence 9, Appli
9	26	96.3	26 15 US-10-463-113-9	Sequence 9, Appli
10	26	96.3	8 US-08-464-363-9	Sequence 39, Appli
11	96.3	96	US-10-463-113-39	Sequence 39, Appli

RESULT 1
US-10-295-903-4
; Sequence 4, Application US/10295903
; Publication No. US20030177512A1
GENERAL INFORMATION:
APPLICANT: AVNER, David B.
TITLE OF INVENTION: METHOD OF GENETICALLY ALTERING AND
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADRESSEER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/295,903
FILING DATE: 18-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6/0/000,189
FILING DATE: 09-JUN-1995
APPLICATION NUMBER: US 08/657,905
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: US 09/227,873
FILING DATE: 11-JAN-1999
ATTORNEY/AGENT INFORMATION:
NAME: SIMKIN, Michele M.

REGISTRATION NUMBER: 34,717
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5399
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-10-295-903-4

RESULT 2
 US-08-464-363-6
 Sequence 6, Application US/09464363
 Publication No. US20030035815A1
 GENERAL INFORMATION:
 APPLICANT: Rogers, Bruce L.
 APPLICANT: Morgenstern, Jay
 APPLICANT: Bond, Julian F.
 APPLICANT: Garman, Richard D.
 APPLICANT: Greenstein, Julia L.
 APPLICANT: Kuo, Mei-chang
 APPLICANT: Morville, Malcolm
 TITLE OF INVENTION: RECOMBITOPE PEPTIDES
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahive & Cockfield
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII TEXT
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,363
 FILING DATE: 05-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/807,529
 FILING DATE: 13-DEC-1991
 APPLICATION NUMBER: US 07/662,276
 FILING DATE: 28-FEB-1991
 APPLICATION NUMBER: US 07/431,565
 FILING DATE: 03-NOV-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragouras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-015CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 109 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-464-363-6

RESULT 3
 US-09-847-208-98
 Sequence 98, Application US/09847208
 Publication No. US2003008219A1
 GENERAL INFORMATION:
 APPLICANT: Saxon, Andrew
 APPLICANT: Zhang, Ke
 APPLICANT: Zhu, Daocheng
 TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
 FILE REFERENCE: U657,00A
 CURRENT APPLICATION NUMBER: US/09/847,208
 CURRENT FILING DATE: 2001-05-01
 NUMBER OF SEQ ID NOS: 177
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 98
 LENGTH: 109
 TYPE: PRT
 ORGANISM: Felis silvestris catus (Cat)
 US-09-847-208-98

RESULT 4
 US-10-245-871-136
 Sequence 136, Application US/10245871
 Publication No. US20030235594A1
 GENERAL INFORMATION:
 APPLICANT: HUMPHREYS, ROBERT
 APPLICANT: XU, MINZHEN
 TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
 FILE REFERENCE: REB-2013
 CURRENT APPLICATION NUMBER: US10/245,871
 CURRENT FILING DATE: 2003-01-09
 PRIOR APPLICATION NUMBER: 10/197,000
 PRIOR FILING DATE: 2002-07-17
 PRIOR APPLICATION NUMBER: 09/396,813
 PRIOR FILING DATE: 1999-09-14
 NUMBER OF SEQ ID NOS: 905
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 136
 LENGTH: 109
 TYPE: PRT
 ORGANISM: Felis domesticus
 US-10-245-871-136

Query Match 100.0%; Score 27; DB 8; Length 109;
 Best Local Similarity 100.0%; Pred. No. 6.5e-18; Length 109;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLIDLDSLTKVNATEPERT 27
 Db 31 FFAVANGNELLIDLDSLTKVNATEPERT 57

RESULT 5
 US-10-463-113-6

Sequence 6, Application US/10463113
 Publication No. US20040057959A1
 GENERAL INFORMATION:
 APPLICANT: Rogers, Bruce L.
 Morgenstern, Jay
 Bond, Julian F.
 Garman, Richard D.
 Greenstein, Julia L.
 Kuo, Mei-chang
 Morville, Malcolm
 TITLE OF INVENTION: RECOMBITOPE PEPTIDES
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahive & Cockfield, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII TEXT
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/463,113
 FILING DATE: 16-Jun-2003
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/807,529
 FILING DATE: 13-Dec-1991
 APPLICATION NUMBER: US 07/662,276
 FILING DATE: 28-Feb-1991
 APPLICATION NUMBER: US 07/431,565
 FILING DATE: 03-Nov-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragoras
 REGISTRATION NUMBER: 36,207
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 109
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-10-463-113-6

RESULT 6
 Query Match 100.0%; Score 27; DB 15; Length 109;
 Best Local Similarity 100.0%; Pred. No. 6.5e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDSLTKNATEPERT 27
 Db 31 FFAVANGNELLIDSLTKNATEPERT 57

RESULT 6
 Sequence 6, Application US/10463113
 Publication No. US20040057959A1
 GENERAL INFORMATION:
 APPLICANT: Rogers, Bruce L.
 Morgenstern, Jay
 Bond, Julian F.
 Garman, Richard D.
 Greenstein, Julia L.
 Kuo, Mei-chang
 Morville, Malcolm
 TITLE OF INVENTION: RECOMBITOPE PEPTIDES
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahive & Cockfield
 STREET: 28 State Street, Suite 510
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:

RESULT 7
 US-10-809-689-32
 Query Match 100.0%; Score 27; DB 15; Length 109;
 Best Local Similarity 100.0%; Pred. No. 6.5e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDSLTKNATEPERT 27
 Db 31 FFAVANGNELLIDSLTKNATEPERT 57

RESULT 7
 US-10-809-689-32
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 Best Local Similarity 100.0%; Pred. No. 6.5e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDSLTKNATEPERT 27
 Db 31 FFAVANGNELLIDSLTKNATEPERT 57

PRIOR FILING DATE: 1999-01-11
 PRIORITY NUMBER: GB/9800445.0
 FILE REFERENCE: 55381010
 CURRENT APPLICATION NUMBER: US/10/809,689
 CURRENT FILING DATE: 2004-03-25
 PRIOR APPLICATION NUMBER: PCT/GB99/00080
 PRIOR FILING DATE: 1998-09-21
 PRIORITY NUMBER: GB/9800445.0
 PRIORITY FILING DATE: 1998-01-09
 PRIORITY NUMBER: GB/9820474.6
 PRIOR FILING DATE: 1998-09-21
 NUMBER OF SEQ ID NOS: 124
 SOFTWARE: Patentin version 3.0
 SEQ ID NO: 32
 LENGTH: 109
 TYPE: PRT
 ORGANISM: Felis catus
 US-10-809-689-32

RESULT 8
 US-08-464-363-9
 Query Match 100.0%; Score 27; DB 16; Length 109;
 Best Local Similarity 100.0%; Pred. No. 6.5e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDSLTKNATEPERT 27
 Db 31 FFAVANGNELLIDSLTKNATEPERT 57

PRIOR FILING DATE: 1999-01-11
 PRIORITY NUMBER: GB/9800445.0
 FILE REFERENCE: REH-2015
 CURRENT APPLICATION NUMBER: US/10/253,286
 CURRENT FILING DATE: 2003-01-13
 PRIOR APPLICATION NUMBER: 10/197,000
 PRIOR FILING DATE: 2002-07-17
 NUMBER OF SEQ ID NOS: 124
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahive & Cockfield
 STREET: 28 State Street, Suite 510
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII TEXT
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,363
 FILING DATE: 05-JUN-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/807,529
 FILING DATE: 13-DEC-1991
 APPLICATION NUMBER: US 07/662,276
 FILING DATE: 28-FEB-1991
 APPLICATION NUMBER: US 07/431,565
 FILING DATE: 03-NOV-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragouras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-015CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 422-4014
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 amino acids
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: Peptide
 FRAGMENT TYPE: Internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 US-10-463-113-9

RESULT 9

Query Match 96.3%; Score 26; DB 8; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.6e-17;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDLSSLTKVNAPER 26
 Db 1 FFAVANGNELLIDLSSLTKVNAPER 26

RESULT 10

Query Match 96.3%; Score 26; DB 15; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.6e-17;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDLSSLTKVNAPER 26
 Db 1 FFAVANGNELLIDLSSLTKVNAPER 26

RESULT 10

US-08-464-363-39

Sequence 39, Application US/08464363
 Publication No. US20030035815A1
 GENERAL INFORMATION:
 APPLICANT: Rogers, Bruce L.
 APPLICANT: Morgenstern, Jay
 APPLICANT: Bond, Julian F.
 APPLICANT: Garman, Richard D.
 APPLICANT: Greenstein, Julia L.
 APPLICANT: Kuo, Mei-chang
 APPLICANT: Morville, Malcolm
 TITLE OF INVENTION: RECOMBITOPE PEPTIDES
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahive & Cockfield, LLP
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII TEXT
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,363
 FILING DATE: 05-JUN-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/807,529
 FILING DATE: 13-DEC-1991
 APPLICATION NUMBER: US 07/662,276
 FILING DATE: 28-FEB-1991
 APPLICATION NUMBER: US 07/431,565
 FILING DATE: 16-Jun-2003
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/807,529
 FILING DATE: 13-DEC-1991
 APPLICATION NUMBER: US 07/662,276
 FILING DATE: 28-FEB-1991
 APPLICATION NUMBER: US 07/431,565
 FILING DATE: 03-NOV-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragouras
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: IMI-015CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 422-4014
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 96 amino acids
 TYPE: amino acid

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; MOLECULE TYPE: protein
; TOPOLOGY: linear
; US-08-464-363-39

; RESULT 11
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; Sequence 39, Application US/10463113
; Publication No. US20040057959A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,113
; FILING DATE: 16-Jun-2003
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; PRIORITY APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mantragoura
; REFERENCE/DOCKET NUMBER: IMI-015CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 743-4214
; INFORMATION FOR SEQ ID NO: 39:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-10-463-113-39

; RESULT 12
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; Best Local Similarity 100.0%; Pkd. No. 3.9e-08; Mismatches 0; Indels 0; Gaps 0;
; Sequence 17, Application US/10463113
; Publication No. US20040057959A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,363
; FILING DATE: 05-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; PRIORITY APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mantragoura
; REFERENCE/DOCKET NUMBER: 36-207
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-464-363-17

; RESULT 13
; Query Match 59.3%; Score 16; DB 8; Length 21;
; Best Local Similarity 100.0%; Pkd. No. 3.9e-08; Mismatches 0; Indels 0; Gaps 0;
; Sequence 17, Application US/10463113
; Publication No. US20040057959A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-463-113-39

; Query Match 95.3%; Score 26; DB 15; Length 96;
; Best Local Similarity 100.0%; Pkd. No. 5.1e-17; Mismatches 0; Indels 0; Gaps 0;
; Sequence 39, Application US/10463113
; Publication No. US20040057959A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-463-113-39

; Query Match 1 FFAVANGELLDISLTKNATKPER 26
; Best Local Similarity 100.0%; Pkd. No. 5.1e-17; Mismatches 0; Indels 0; Gaps 0;
; Sequence 1 FFAVANGELLDISLTKNATKPER 26
; Publication No. US20040057959A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-463-113-39

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TITLE OF INVENTION: RECOMBITOPE PEPTIDES
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahive & Cockfield, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/463,113
 FILING DATE: 16-Jun-2003
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/807,529
 FILING DATE: 13-DEC-1991
 APPLICATION NUMBER: US 07/662,276
 FILING DATE: 28-FEB-1991
 APPLICATION NUMBER: US 07/431,565
 FILING DATE: 03-NOV-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragouras
 REGISTRATION NUMBER: 36,207
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEX/FAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-10-463-113-17

Query Match 59.3%; Score 16; DB 15; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.9e-08; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; MisMatches 0; Length 21;

Qy 1 FFAVANGNELLDSL 16
 Db 6 FFAVANGNELLDSL 21

RESULT 14
 US-08-464-363-19
 Sequence 19, Application US/08464363
 Publication No. US20040057959A1

GENERAL INFORMATION:
 APPLICANT: Rogers, Bruce L.
 APPLICANT: Morgenstern, Jay
 APPLICANT: Bond, Julian F.
 APPLICANT: Garman, Richard D.
 APPLICANT: Greenstein, Julia L.
 APPLICANT: Kuo, Mei-chang
 APPLICANT: Morville, Malcolm
 TITLE OF INVENTION: RECOMBITOPE PEPTIDES
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahive & Cockfield, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/463,113
 FILING DATE: 16-Jun-2003
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/807,529
 FILING DATE: 13-DEC-1991
 APPLICATION NUMBER: US 07/662,276
 FILING DATE: 28-FEB-1991
 APPLICATION NUMBER: US 07/431,565
 FILING DATE: 03-NOV-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragouras
 REGISTRATION NUMBER: 36,207
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-464-363-19

RESULT 15
 US-10-463-113-19
 Sequence 19, Application US/10463113
 Publication No. US20040057959A1

GENERAL INFORMATION:
 APPLICANT: Rogers, Bruce L.
 APPLICANT: Morgenstern, Jay
 APPLICANT: Bond, Julian F.
 APPLICANT: Garman, Richard D.
 APPLICANT: Greenstein, Julia L.
 APPLICANT: Kuo, Mei-chang
 APPLICANT: Morville, Malcolm
 TITLE OF INVENTION: RECOMBITOPE PEPTIDES
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lahive & Cockfield, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/463,113
 FILING DATE: 16-Jun-2003
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/807,529
 FILING DATE: 13-DEC-1991
 APPLICATION NUMBER: US 07/662,276
 FILING DATE: 28-FEB-1991
 APPLICATION NUMBER: US 07/431,565
 FILING DATE: 03-NOV-1989
 ATTORNEY/AGENT INFORMATION:

NAME: Amy B. Mandragourab
REGISTRATION NUMBER: 36 207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-463-113-19

Query Match 55.6%; Score 15; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 LDLSITKRNATPER 26
||| ||| ||| ||| ||| |||
Db 1 LDLSITKRNATPER 15

Search completed: October 18, 2005, 14:01:48
Job time : 179 secs

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Name=3; Synonyms=CH2ST, Truncated; ISOID=P30440-3; Sequence=VSP_004248; -I- TISSUE SPECIFICITY: The long form is preferentially expressed in the salivary gland, while the short form is preferentially expressed in the skin.

-I- ALLERGEN: Causes an allergic reaction in human. Major allergen produced by the domestic cat.

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EMBL; M77341; ARCA1616.1; -.

EMBL; X62478; CARA4345.1; -.

PIR; B53283; B53283.

PIR; C56413; C56413.

PIR; JC1127; JC1127.

InterPro; IPR005038; Uteroglobin_sfup.

Allergen; Alternative splicing; Direct protein sequencing;

Glycoprotein; Polymorphism; Signal.

Signal; CHAIN 1 17 Major allergen I polypeptide chain 2.

Carbohd 50 50 N-linked (GlcNAc).

VARSPLIT 82 109 TRISSKIDCMGRAVONTVEDKLNTLGR -> PSTNIAWVK

QRTS (in isoform 3).

/FTId=VSP_004248.

/FTId=VSP_004249.

VARIANT 72 72 I -> L (in CH2LV).

VARIANT 72 72 I -> V (in CH2SV).

VARIANT 74 75 RV -> KP (in CH2SV).

M -> T (in CH2LV).

Q -> E (in CH2SV).

N -> K (in CH2SV).

C -> F (in Ref. 3).

CONFFLICT 24 24 F -> T (in Ref. 3).

CONFLICT 32 32 SEQUENCER 109 AA; 11854 MW; 857FB9CD7036CB9 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 109; Best Local Similarity 100.0%; Pred. No. 5 2e-20; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 31 FFAVANGNELLALDLSLTKVNATEPERT 57

RESULT 2

06R184 ID OGR184 PRELIMINARY; PRT; 509 AA.

AC OGR184; 06R184;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DR FARR1, protein (Fragment).

GN Name=FARR1;

OS Zygosaccharomyces rouxii (Candida magii).

OC Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetidae; Saccharomycetaceae; Zygosaccharomyces.

NCBI_TaxID=4956;

[1] SEQUENCE FROM N.A.

RC STRAIN=CBS 732;

RA Wolfe K.H.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY496363; ARRA88365.1; -.

NON_TER 509 509 SEQUENCE FROM N.A.

RN 509 AA; 58713 MW; BAB6F2FB4B901589 CRC64;

RA

RP

SEQUENCE FROM N.A.

RC

RA

RL

DR

FT NON_TER 509 509 SEQUENCE FROM N.A.

SQ SEQUENCE FROM N.A.

Query Match 29.6%; Score 8; DB 2; Length 509; Best Local Similarity 100.0%; Pred. No. 8.8; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

Q9KG69 ID Q9KG69 PRELIMINARY; PRT; 77 AA.

AC Q9KG69;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE BH024 protein.

OrderedLocusName=BH0244;

OS Bacillus halodurans.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=86655;

[1] SEQUENCE FROM N.A.

RC STRAIN=C-125;

RA MEDLINE=0512882; PubMed=11058132; DOI=10.1093/nar/28.21.4317;

RA Takami H., Nakane R., Takaki T., Maeno G., Sasaki R., Matsui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kubara S.,

RA Horikoshi K.;

RT "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with *Bacillus subtilis*."

RL Nucleic Acids Res. 28:4317-4331(2000).

DR EMBL; AP001507; BAB03963.1; -.

DR PIR; DB3680; DB3680.

KW Complete proteome.

SEQUENCE 77 AA; 9511 MW; F9BEC3529F5CE320 CRC64;

Query Match 25.9%; Score 7; DB 2; Length 77; Best Local Similarity 100.0%; Pred. No. 17; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 ELLIDS 30

RESULT 4

Q8KLB4 ID Q8KLB4 PRELIMINARY; PRT; 100 AA.

AC Q8KLB4;

DT 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DR Hypothetical protein yh014.

GN Name=yh014;

OS Rhizobium etli.

OC Plasmid symbiotic plasmid p42d.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.

OK NCBI_TaxID=29449;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=CFW42;

RA MEDLINE=91193195; PubMed=2013564;

RA Girard M.L., Flores M., Brom S., Romero D., Palacios R., Davila G.;

RA "Structural complexity of the symbiotic plasmid of Rhizobium

leguminosarum bv. phaseoli."

RL Bacteriol. 173:2411-2419(1991).

[2] SEQUENCE FROM N.A.

RC STRAIN=CFW42;

RA MEDLINE=97419521; PubMed=9274036;

RA Ramirez-Romero M.A., Bustos P., Girard L., Rodriguez O.,

RA Cevallos M.A., Davila G.;

		KW	Hypothetical protein.
		SQ	SEQUENCE 106 AA; 10471 MW; 1152A36A14B66D80 CRC64;
RT	"Sequence, localization and characteristics of the replicator region of the symbiotic plasmid of <i>Rhizobium etli</i> ."		
RL	Microbiology 143:2825-2831(1997).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CFN42;		
RX	MDLINE=22309397; PubMed=12421308;		
RA	Quintero V., Cevallos M.A., Davila G.;		
RT	"A site-specific recombinase (RinQ) is required to exert incompatibility towards the symbiotic plasmid of <i>Rhizobium etli</i> ."		
RL	Mol. Microbiol. 46:1023-1032(2002).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CFN42;		
RA	Ramirez M.A., Bustos P., Girard L., Rodriguez O., Cevallos M.A.,		
RA	Davila G.;		
RL	Submitted: (NOV-1999) to the EMBL/GenBank/DBJ databases.		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CFN42;		
RA	Quintero V., Bustos P., Davila G.;		
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.		
RN	[6]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CFN42;		
RA	Gonzalez V., Bustos P., Medrano-Soto A., Ramirez-Romero M.A.,		
RA	Ramero D., Salgado H., Hernandez-Gonzalez I., Hernandez-Celis J.C.,		
RA	Quintero V., Girard L., Rodriguez O., Flores M., Cevallos M.A.,		
RA	Collado-Vieira J., Davilla G.;		
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.		
RN	[7]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CFN42;		
RA	Ramero D., Salgado H., Hernandez-Gonzalez I., Hernandez-Celis J.C.,		
RA	Quintero V., Girard L., Rodriguez O., Flores M., Cevallos M.A.,		
DR	EMBL; U80928; NM_005832.1; -;		
RN	Hypothetical protein; Plasmid		
SQ	SEQUENCE 100 AA; 11433 MW; 6179A83270F7P4B CRC64;		
Query Match	25.9%; Score 7; DB 2; Length 100;		
Beet Local Similarity	100.0%; Pred. No. 22;		
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	10 LLDDSL 16		
Db	84 LLDDSL 90		
RESULT 5			
06ZDG2	PRELIMINARY; PRT; 106 AA.		
ID	06ZDG2		
AC	06ZDG2;		
DT	05-JUL-2004 (TREMBL; 27, Last sequence update)		
DT	05-JUL-2004 (TREMBL; 27, Last annotation update)		
DB	Hypothetical protein P0451G12.25 (Hypothetical protein 04511_005_3).		
DE	Name=P0451G12.25; Synonyms=04511_005_3;		
OS	Oryza sativa (japonica cultivar-group).		
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Bihartoidea; Oryzeae; Oryza.		
NCBI_TaxID	39947;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Sasaki T., Matsumoto T., Yamamoto K.;		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Sasaki T., Matsumoto T., Yamamoto K.;		
RA	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; AP004395; BAD09348.1; -.		
DR	EMBL; AP004154; BAD09194.1; -.		
RESULT 6			
06PYC6	PRELIMINARY; PRT; 134 AA.		
ID	06PYC6		
AC	06PYC6;		
DT	05-JUL-2004 (TREMBL; 27, Last sequence update)		
DT	05-JUL-2004 (TREMBL; 27, Last annotation update)		
DB	Bacteriorhodopsin (Fragment).		
GN	Name=bop;		
OS	Natrinema ajinweensis.		
OC	Archaeae; Euryarchaeota; Halobacteria; Halobacteriales;		
OK	NCBI_TaxID=222984;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=AJ12, AJ13, and AJ11;		
RA	Xu X.W., Wu M.;		
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ1570920; AAS87572.1; -.		
DR	EMBL; AY570921; AAS87573.1; -.		
DR	HSSE; P02945; IKG9.		
DR	GO; GO:0015020; C:membrane; IEA.		
DR	GO; GO:005216; F:ion channel activity; IEA.		
DR	GO; GO:0005811; P:ion transport; IEA.		
DR	InterPro; IPR001425; Bac_rhodopsin.		
DR	PFAM; PF01036; Bac_rhodopsin_1.		
DR	PRINTS; PRO0251; BACTERIOPSPIN.		
DR	PROSITE; PS00237; BACTERIAL_OPSIN_RBT; 1.		
FT	NON_TER 1 1		
FT	NON_TER 134 134		
SQ	SEQUENCE 134 AA; 14303 MW; 86AB51BC66DAAFFAC CRC64;		
Query Match	25.9%; Score 7; DB 2; Length 134;		
Beet Local Similarity	100.0%; Pred. No. 29;		
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	10 LLDDSL 16		
Db	3 LLDDSL 9		
RESULT 7			
Q6DMV1	PRELIMINARY; PRT; 134 AA.		
ID	Q6DMV1		
AC	Q6DMV1;		
DT	25-OCT-2004 (TREMBL; 28, Created)		
DT	25-OCT-2004 (TREMBL; 28, Last sequence update)		
DT	25-OCT-2004 (TREMBL; 28, Last annotation update)		
DB	Hypothetical protein.		
OS	Streptococci prophages.		
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
OC	Streptococcus.		
OC	NCBI_TaxID=1314;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=2812A;		
RA	MEDLINE=2283765; PubMed=12959402; DOI=10.1089/1076290322286445;		
RA	Santacatalina M., Iannelli F., Cascone C., Campanile F., Oggioni M.R.,		
RA	Stefani S., Pozzi G.;		
RA	"The novel conjugative transposon Tn1207-3 carries the macrolide		

RT efflux gene *mef(A)* in *Streptococcus pyogenes*.";
 RL "Microb. Drug Resist. 9:243-247(2003).";
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2812A;
 RA Santabarbara M., Iannelli F., Cascone C., Stefani S., Pozzi G.,;
 DR Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 KW EMBL, AY55002; RAT7374.1; -.
 SQ SEQUENCE 134 AA; 15373 MW; 897916A18372A242 CRC64;
 Query Match 25.9%; Score 7; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy ||||||| 11 LUDLSL 17
 Db 25 LUDLSL 31

RESULT 8

Q9X302 PRELIMINARY; PRT; 198 AA.
 AC Q9X302;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 RC BACILLUS ANTHRACIS.
 OC Plasmid virulence plasmid pXO1.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TAXID=1392;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=STEERNE;
 RX MEDLINE=99445483; PubMed=10515943;
 RA Okinaka R.T., Cloud K.M., Hampton R., Hoffmaster A.R., Hill K.R.,
 RA Keim P., Koehler T.M., Lankie G., Kumano S., Mahillon J., Mander D.,
 RA Martinez Y., Riche D., Svenson R., Jackson P.J.;
 RT "Sequence and organization of pXO1, the large *Bacillus anthracis*
 RT Plasmid harboring the anthrax toxin genes.;"
 RL J. Bacteriol. 181:6509-6515(1999).
 DR EMBL; APO03404; ADD32335.1; -.
 DR PIR; G59094; G59094.
 KW Plasmid.
 SQ SEQUENCE 198 AA; 22859 MW; D76737FD81C43C9D CRC64;
 Query Match 25.9%; Score 7; DB 2; Length 198;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy ||||||| 8 NEUILLD 14
 Db 150 NEUILLD 156

RESULT 9

Q9CR_HAL54 PRELIMINARY; PRT; 250 AA.
 ID Q9CR_HAL54 STANDARD; PRT; 250 AA.
 AC 093740;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 05-JUL-2004 (Rel. 40, Last sequence update)
 DR Bacteriorhodopsin (BR).
 DE Bacteriorhodopsin (BR).
 GN Name=brp;
 OS Halobacterium sp. (strain arg-4).
 OC Archaea, Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 RN NCBI_TAXID=160432;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99096913; PubMed=9878996; DOI=10.1006/jmbi.1998.2285;
 RA Ihara K., Umemura T., Katagiri I., Kitajima-Ihara T., Sugiyama Y.,

RA Kimura Y., Mukohata Y.;
 RT "Evolution of the archaeal rhodopsins: evolution rate changes by gene
 RT duplication and functional differentiation.";
 RT J. Mol. Biol. 285:163-174(1999).
 CC -I- FUNCTION: Light-driven proton pump.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: Belongs to the archaeal/bacterial/fungal opsin family.
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 CC
 DR EMBL; AB009620; BAM75200.1; -.
 DR HSSP; P02345; IBRD.
 DR InterPro; IPR001425; Bac rhodopsin.
 DR Pfam; PF01036; Bac rhodopsin.
 DR PROSITE; PS00251; BACTERIAL_OPSIN.
 DR PROSITE; PS0050; BACTERIAL_OPSIN_1; 1.
 DR PROSITE; PS00327; BACTERIAL_OPSIN_RET; 1.
 DR Hydrogen ion transport; Ion transport; Photoreceptor; Retinal protein;
 KW Transmembrane.
 FT DOMAIN 1 18
 FT TRANSMEM 19 37
 FT DOMAIN 38 51
 FT TRANSMEM 52 70
 FT DOMAIN 71 86
 FT TRANSMEM 87 104
 FT DOMAIN 105 115
 FT TRANSMEM 116 135
 FT DOMAIN 136 142
 FT TRANSMEM 143 162
 FT DOMAIN 163 180
 FT TRANSMEM 181 199
 FT DOMAIN 200 210
 FT TRANSMEM 213 232
 FT DOMAIN 233 250
 FT SITE 93 93
 FT BINDING 225 225
 SQ SEQUENCE 250 AA; 27041 MW; B7D3373506FD275 CRC64;
 Query Match 25.9%; Score 7; DB 1; Length 250;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy ||||||| 10 LUDLSL 16
 Db 101 LUDLSL 107

RESULT 10

Q6FCV6 PRELIMINARY; PRT; 255 AA.
 ID Q6FCV6
 AC Q6FCV6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DR Survival protein (acid phosphatase) (EC 3.1.3.2).
 DE Name=scrB; Order=scrB; AC=ACI01227;
 OS Acinetobacter sp. (strain ADP1).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TAXID=62977;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barbe V., Vallenet D., Foncknechten N., Kreimeyer A., Oztas S.,
 RA Labarre L., Crueviller S., Robert C., Duprat S., Wincker P.,
 RA Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.,
 RT "unique features revealed by the genome sequence of *Acinetobacter* sp.
 ADP1, a versatile and naturally transformation competent bacterium.";

RL Nucleic Acids Res. 0:0-0(2004).
 DR EMBL: CR443861; CAG68103-1; -.
 DR GO: GO:0003933; F-acid phosphatase activity; IEA.
 DR Interpro; IPR02828; Sure.
 DR PFAM; PF01975; Sure; 1.
 DR PRODOM; PD005378; Sure; 1.
 DR TIGRFAMS; TIGR00087; sure; 1.
 DR KW Complete proteome.
 SQ SEQUENCE 255 AA; 27574 MW; C4B04235BP82A46 CRC64;
 Query Match Best Local Similarity 100.0%; Pred. No. 51; Length 255;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FFAVANG 7
 Db 224 FFAVANG 230

RESULT 11

PRELIMINARY; PRT; 273 AA.
 ID QCP5B
 ID QCP5B; PRELIMINARY; PRT; 273 AA.
 AC QCP5B;
 DT 25-OCT-2004 (TREMBrel. 28, Created)
 DT 25-OCT-2004 (TREMBrel. 28, last sequence update)
 DT 25-OCT-2004 (TREMBrel. 28, last annotation update)
 DE Similar to sp|P26754 Saccharomyces cerevisiae YNL312w RFA2 DNA
 DE replication factor A.
 GN ORPNAME=KLIA0B073489;
 OS Kluyveromyces lactis NRRL Y-1140.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetidae; Saccharomyctaceae; Kluyveromyces.
 OC NCBI_TaxID=284590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRL Y-1140;
 RG Genolouvres;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Caaregola S.,
 RA Lafontaine I., de Montigny J., Marcot C., Neuveglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bluykaeten C.,
 RA Boisrame A., Boyer J., Cattolico L., Confinioleri F., de Darvira A.,
 RA Despont L., Fabre E., Faucheu H., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Henneguin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Keraudr A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicastri J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Svennene D., Tekata F., Wasolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivkovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts.."
 RT Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRL Y-1140;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ database.
 DR EMBL: CR392125; CAG99568.1; -.
 DR GO: GO:0003675; F-nucleic acid binding; IEA.
 DR Interpro; IPR008934; Nucleic acid_OB.
 DR Interpro; IPR04325; tRNA_anti.
 DR PF01336; tRNA_antI_1.
 SQ SEQUENCE 273 AA; 30347 MW; 4121F346314942BD CRC64;
 Query Match Best Local Similarity 100.0%; Pred. No. 54; Length 273;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FAVANG 8
 Db 174 FAVANG 180

RESULT 12

PRELIMINARY; PRT; 279 AA.
 ID P73885
 ID P73885; PRELIMINARY; PRT; 279 AA.
 AC P73885;
 DT 01-FEB-1997 (TREMBrel. 02, Created)
 DT 01-FEB-1997 (TREMBrel. 02, last sequence update)
 DT 01-FEB-1997 (TREMBrel. 24, last annotation update)
 DE Sir267 protein.
 GN OrderedLocusName=SL0267;
 OS Synechocystis sp. (strain PCC 6803);
 OC Synechocystis; Cyanobacteria; Chroococcales; Synechocystis.
 OC NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC6803;
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirosewa M., Sugiyama M., Sasamori S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakaki N., Naruo K., Okumura S.,
 RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.,";
 RL DNA Res. 3:105-116 (1996).
 DR EMBL: D99910; BAA17949.1; -.
 DR PIR; S75087; S75087.
 DR HSSP; 031743; IPU.
 DR GO; GO:0005525; F-GTP binding; IEA.
 DR Interpro; IPR005209; GTP-binding.
 DR Interpro; IPR06073; GTP1_OBG.
 DR Interpro; IPR02917; MMR_F5R1.
 DR PFAM; PF01926; MMR_HSR1; 1.
 DR PRINTS; PR00226; GTP1_OBG.
 DR TIGRFAMS; TIGR00650; MG412; 1.
 DR KW Complete proteome.
 SQ SEQUENCE 279 AA; 31201 MW; 9AA603118D77763 CRC64;
 Query Match Best Local Similarity 100.0%; Pred. No. 55; Length 279;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 LLDSL 16
 Db 213 LLDSL 219

RESULT 13

PRELIMINARY; PRT; 303 AA.
 ID 064761
 ID 064761; PRELIMINARY; PRT; 303 AA.
 AC 064761;
 DT 01-AUG-1998 (TREMBrel. 07, Created)
 DT 01-AUG-1998 (TREMBrel. 07, last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, last annotation update)
 DE Putative phosphatidylinoitol-glycan synthase.
 GN Name=at2934980;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Spermatophytina; Magnoliophyta; eudicots; core eudicots; rosids; eudicots II; Brassicales; Brassicaceae; Arabidopsis.
 OC europa_II; Brassicales; Brassicaceae; Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rounseley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C., Somerville C.R., Venter J.C.;
 RA Sykes S.M., Kaul S., Mason T.M., Keiravage A.R., Adams M.D.,
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Town C.D., Kaul S.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AAC04238; AAC12837.1; -.

Query Match 25.9%; Score 7; DB 2; Length 303;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLDDSL 16
 Db 89 LLDDSL 95

|||||||

RESULT 14

Q8KYR1 PRELIMINARY; PRT; 310 AA.

ID Q8KYR1
 AC 08KYR1;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DB Hypothetical protein BXA0045.
 GN Name=BXA0045;
 OS Bacillus anthracis str. A2012.
 OC Plasmid pXO1.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=191218;
 RN [1]
 RP SEQUENCE FROM N A.
 RC STRAIN=A2012;
 RX MEDLINE=22061436; PubMed=12004073; DOI=10.1126/science.1071837;
 RA Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
 RA Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
 RA Keim P., Fraser C.M.;
 RT "Comparative Genome Sequencing for Discovery of Novel Polymorphisms in
 RT *Bacillus anthracis*," Sequencing for Discovery of Novel Polymorphisms in
 RL Science 296:12028-2033 (2002).
 DR EMBL; AE001190; AAM2001.1; --.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 310 AA; 36423 MW; 716F21DB64CFE274 CRC64;
 Query Match 25.9%; Score 7; DB 2; Length 310;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NEILDL 14
 Db 262 NEILDL 268

|||||||

RESULT 15

Q6EZX1 PRELIMINARY; PRT; 310 AA.

ID Q6EZX1;
 AC 06EZX1;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DB Hypothetical protein.
 GN OrderedLocusNames=GBAA_pXO1_0045;
 OS Bacillus anthracis.
 OC Plasmid pXO1; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1392;
 RN [1]
 RP SEQUENCE FROM N A.
 RC STRAIN=Ames / isolate 0581;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RT "Bacillus anthracis comparative genomics,"

RL Submitted (MAY-2004) to the EMBL/GenBank/DBBJ databases.
 DR EMBL; AE017336; AAT28786.2; --.
 DR TIGR; GBAA_pXO1_0045; --.
 KW Complete proteome.
 SQ SEQUENCE 310 AA; 36423 MW; 716F21DB64CFE274 CRC64;
 Query Match 25.9%; Score 7; DB 2; Length 310;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 NEILDL 14
 Db 262 NEILDL 268

|||||||

Search completed: October 18, 2005, 13:47:25
 Job time : 182 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 13:37:20 ; Search time 39 Seconds
(without alignments)
66.612 Million cell updates/sec

Title: US-09-662-784-6_COPY_33_59

Perfect score: 27

Sequence: 1 FFAVANGNELLIDSLTKUNATEPERT 27

Scoring table: OLIGO

Searched: Gapop 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 79.1

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	27	100.0	107	JC1127	major allergen chain 2 precursor, short form - cat
2	27	100.0	109	C56413	major allergen chain 2 precursor, short form - cat
3	25.9	77	2	DB3680	hypothetical protein
4	7	25.9	198	G59094	hypothetical protein
5	7	25.9	250	T50677	bacteriorhodopsin
6	7	25.9	279	S75087	hypothetical protein
7	7	25.9	303	T00479	probable phosphatase
8	7	25.9	455	B86722	biotin carboxylate
9	7	25.9	524	S44982	flagellin - Shigella
10	6	22.2	87	B82678	hypothetical protein
11	6	22.2	100	E90993	hypothetical protein
12	6	22.2	106	1 KIRPA	Ig kappa chain C region
13	6	22.2	107	D72598	hypothetical protein
14	6	22.2	112	2 T09060	hypothetical protein
15	6	22.2	118	H90453	hypothetical protein
16	6	22.2	127	2 A33894	chorismate mutase
17	6	22.2	147	2 AC2066	hypothetical protein
18	6	22.2	150	2 F9703	transcription regulator
19	6	22.2	155	2 I45513	interleukin-2 precursor
20	6	22.2	155	2 S11888	interleukin-2 precursor
21	6	22.2	160	T23995	hypothetical protein
22	6	22.2	161	2 G86541	CT260 hypothetical protein
23	6	22.2	161	2 H72082	conserved hypothetical protein
24	6	22.2	170	2 H72039	dihydrofolate reductase
25	6	22.2	170	2 E86585	dihydrofolate reductase
26	6	22.2	174	2 F81411	conserved hypothetical protein
27	6	22.2	175	2 B97974	degenerate transposon
28	6	22.2	191	2 C72411	Holliday Junction
29	6	22.2	199	2 H87416	phosphoglycerate kinase

ALIGNMENTS

RESULT 1

JC1127
major allergen chain 2 precursor, short form - cat

C;Species: *Felis silvestris catus* (domestic cat)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: JC1127; Craig, S.; Pollock, J.; Yu, X.B.; Morgenstern, J.P.; Rogers, B.L.

Gene 113, 263-268, 1992

A;Title: Expression and genomic structure of the genes encoding FdI, the major allergen

A;Reference number: JC1126; MUID:92241678; PMID:1572548

A;Accession: JC1127; MUID:92241678; PMID:1572548

A;Molecule type: DNA

A;Cross-references: UNIPROT:P30440; GB:X62478; NID:9395406; PID:CAA44345.1; PID:9195407

A;Experimental source: skin

C;Genetics:

A;Gene: Ch2

A;Residues: 21/1; 81/3

C;Keywords: glycoprotein

F;18-107/Product: major allergen chain 2, short form #status predicted <SIG>

F;18-107/Domain: signal sequence #status predicted <MAT>

F;50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 27; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 1; 4e-0; Mismatches 0; Indels 0; Gaps 0;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDSLTKUNATEPERT 27
Db 31 FFAVANGNELLIDSLTKUNATEPERT 57

RESULT 2

C56413
major allergen chain 2 precursor - cat

C;Species: *Felis silvestris catus* (domestic cat)

C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004

C;Accession: C56413; JC1145

R;Morgenstern, J.P.; Griffith, I.J.; Brauer, A.W.; Rogers, B.L.; Bond, J.P.; Chapman, M

Proc. Natl. Acad. Sci. U.S.A., 88, 9610-9614, 1991

A;Title: Amino acid sequence of FdI, the major allergen of the domestic cat: protein

A;Reference number: A56413; MUID:92052157; PMID:1946388

A;Accession: C56413

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-109 <MRN>

A;Cross-references: UNIPROT:P30440; GB:X62478; NID:9163822; PID:9163823

R;Griffith, I.J.; Craig, S.; Pollock, J.; Yu, X.B.; Morgenstern, J.P.; Rogers, B.L.

Gene 113, 263-268, 1992

A;Title: Expression and genomic structure of the genes encoding FdI, the major allergen

A;Reference number: JC1126; MUID:92241678; PMID:1572548

A;Accession: JC1145

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 18-109 <GRI>

A;Experimental source: salivary gland

C;Keywords: glycoprotein

F;1-17/Domain: signal sequence #status predicted <SRG> #status predicted

Query Match 100.0%; Score 27; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.4e-20;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLIDSLTKVNAEPERT 27

Db 31 FFAVANGNELLIDSLTKVNAEPERT 57

RESULT 3

D83680 hypothetical protein BH0244 [imported] - *Bacillus halodurans* (strain C-125)

C;Species: *Bacillus halodurans*

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C;Accession: D83680

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: D83680

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-77 <STO>

A;Cross-references: UNIPROT:Q9KQ69; GB:AP001507; GB:BA000004; NID:910172612; PIDN:BA039

A;Experimental source: strain C-125

C;Genetics: BH0244

Query Match 25.9%; Score 7; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 3; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 S81LDSL 15

Db 24 LLLDLDS 30

RESULT 4

G59094 hypothetical protein px01-31 - *Bacillus anthracis* virulence plasmid px01

C;Species: *Bacillus anthracis*

C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004

C;Accession: G59094

R;Okinaka, R.I.; Cloud, K.; Hampton, O.; Hofmaster, A.R.; Hill, K.K.; Keim, P.; Koehler

J. Bacteriol. 181, 6509-6515, 1999

A;Title: Sequence and organization of px01, the large *Bacillus anthracis* plasmid harboring

A;Reference number: A59091; MUID:9445483; PMID:10515943

A;Accession: G59094

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-198 <OKI>

A;Cross-references: UNIPROT:Q9X302; GB:AF065404; NID:94894216; PIDN:AAD32335.1; PID:9489

A;Experimental source: strain Sterne

C;Genetics: px01-31

C;Species: *Bacillus anthracis* virulence plasmid px01 hypothetical protein px01-31

Query Match 25.9%; Score 7; DB 2; Length 198;

Best Local Similarity 100.0%; Pred. No. 7.3; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NELLDL 14

Db 150 NELLDL 156

RESULT 5

T50677 bacteriorhodopsin [similarity] - "Haloterrigena" sp. (strain arg-4)

C;Species: "Haloterrigena" sp.

A;Variety: strain arg-4

C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000

C;Accession: T50677

R;Ihara, K.; Umemura, T.; Katagiri, I.; Kitajima-Ihara, T.; Sugiyama, Y.; Kimura, Y.; Mu

J. Mol. Biol. 285, 163-174, 1999

A;Title: Evolution of the archaeal rhodopsins: Evolution rate changes by gene duplication

A;Reference number: Z22703; MUID:99096913; PMID:9878396

A;Accession: T50677

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-250 <THA>

A;Cross-references: EMBL:AB009620; PIDN:BA75200.1

C;Genetics:

A;Gene: bop

C;Superfamily: bacteriorhodopsin

C;Keywords: chromoprotein; photoreceptor; retinal; transmembrane protein

F;225/Binding site: retinal(Lys) (covalent) #status predicted

Query Match 25.9%; Score 7; DB 2; Length 250;

Best Local Similarity 100.0%; Pred. No. 9.1; Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLDL 16

Db 101 LLLDL 107

RESULT 6

S75087 hypothetical protein slr0267 - *Synechocystis* sp. (strain PCC 6803)

C;Species: *Synechocystis* sp.

C;Accession: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S75087

R;Kameko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asami, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Matanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

B;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S75087

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-279 <OKN>

A;Cross-references: UNIPROT:P73885; EMBL:D90910; GB:AB001339; NID:91652956; PIDN:BA1794

C;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Superfamily: conserved hypothetical protein MG442

Query Match 25.9%; Score 7; DB 2; Length 279;

Best Local Similarity 100.0%; Pred. No. 10; Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLDL 16

Db 213 LLLDL 219

RESULT 7

T00479 probable phosphatidylinositol-glycan synthase [imported] - *Arabidopsis thaliana*

C;Alternate names: hypothetical protein F1913.21

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

R;Rounseley, S.D.; Lin, K.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

submitted to the EMBL Data Library, April 1998

C;Description: *Arabidopsis thaliana* Chromosome II BAC F1913 genomic sequence.

A;Reference number: Z14160
 A;Accession: T00479
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-303 <ROU>
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsey, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Taiton, L.;
 euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A64420; MUID:20083487; PMID:10617197
 A;Accession: B841763
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-303 <STO>
 A;Cross-references: GB:AE002093; NID:93033393; PIDN:AC12837.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g34980; F1913.21
 A;Map position: 2

Query Match 25.9%; score 7; DB 2; Length 524;
 Best Local Similarity 100.0%; Pred. No. 18; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LUDLISL 16
 Db 89 LUDLISL 95

RESULT 8

B86722 biotin carboxylase (EC 6.3.4.14) [imported] - *Lactococcus lactis* subsp. *lactis* (strain 1
 C;Species: *Lactococcus lactis* subsp. *lactis* (strain 1
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C;Accession: B86722
 R;Bolotin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarrie, K.; Weissenbach, J.; Ehrl
 Genome Res. 11, 731-753, 2001
 A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* se
 A;Reference number: A86625; MUID:21235186; PMID:11337471
 A;Accession: B86722
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-55 <STO>
 A;Cross-references: UNIPROT:Q9CHF3; GB:AE005176; PIDN:91273697; PIDN:AAK04876.1; GSPDB:
 A;Experimental source: strain IL1403
 C;Genetics:
 A;Gene: accC
 C;Superfamily: biotin carboxylase; biotin carboxylase homology
 C;Keywords: ligase

Query Match 25.9%; score 7; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 16; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VANGNEL 10
 Db 316 VANGNEL 322

RESULT 9

44982 flagellin - *Shigella sonnei*
 C;Species: *Shigella sonnei*
 C;Accession: S44982; S44981
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S44982; S44981
 R;Tomino, A.; Mahmud, M.A.H.; Mukaihara, T.; Enomoto, M.
 Mol. Microbiol. 12, 277-285, 1994
 A;Title: Molecular characterization of intact, but cryptic, flagellin genes in the genus
 A;Reference number: S44980; MUID:94335647; PMID:8057852
 A;Accession: S44982
 A;Status: preliminary

A;Molecule type: DNA
 A;Residues: 1-524 <TOM>
 A;Cross-references: UNIPROT:Q09012; EMBL:D16821; NID:9391893; PIDN:BAA04095.1; PID:939185
 C;Superfamily: flagellin

Query Match 25.9%; Score 7; DB 2; Length 524;
 Best Local Similarity 100.0%; Pred. No. 18; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LTKNNT 22
 Db 196 LTKNNT 202

RESULT 10

B86778 hypothetical protein XP1461 [imported] - *Xylella fastidiosa* (strain 9a5c)
 C;Species: *Xylella fastidiosa*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: B86778
 R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A;Reference number: A82515; MUID:20365717; PMID:1091047
 A;Accession: B82678
 A;Note: For a complete list of authors see reference number A59328 below
 A;Status: preliminary
 A;Accession: B82678
 A;Molecule type: DNA
 A;Residues: 1-87 <SIM>
 A;Cross-references: UNIPROT:Q9PDBB; GB:AE003976; GB:AB003849; NID:99106479; PIDN:AAFP8427(
 A;Experimental source: strain 9a5c
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Accencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bruno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrasco, D.M.; Carter, H
 as Neto, E.; Docena, C.; El-Dorry, H.; Pacinani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramme, F.E.; Laigr
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.M.; Marques, M.V.; Martins, E
 A;Authors: Martins, E.M.F.; Matsukawa, A.Y.; Menck, J.; Miracco, E.C.; Mirak, C.Y.,
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
 Rodriguez, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A;Authors: da Silva, F.R.; da Silva, A.M.; Silva, G.; Santelli, R.V.; da Silveira, M.;
 M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A;Reference number: A59328
 A;Contents: annotation
 C;Genetics:
 A;Gene: XP1461

Query Match 22.2%; Score 6; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 36; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NEILLD 13
 Db 2 NEILLD 7

RESULT 11

E90033 hypothetical protein orf100 [imported] - *Guillardia theta* nucleomorph
 C;Species: nucleomorph *Guillardia theta*
 A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C;Accession: E90033
 R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
 Nature 410, 1091-1096, 2001
 A;Title: The highly reduced genome of an enslaved algal nucleus.
 A;Reference number: A99082; MUID:11323671; PMID:11323671
 A;Accession: E90093
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-100 <DOU>
 A;Cross-references: UNIPROT:Q98RS0; GB:AF165818; NID:913794502; PIDN:AAK39877.1; GSPDB:G

Q:Gene: orf100
 A:Map position: 1
 A:Genome: nucleomorph
 C:Keywords: nucleomorph

Query Match 22.2%; Score 6; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0;
 Qy 10 LLUDLS 15
 Db 40 LLUDLS 45

RESULT 12
 KIRTA
 Ig kappa chain C region (allele a) - rat
 C-Species: *Rattus norvegicus* (Norway rat)
 C-Accession: 18-Aug-1982 #sequence_revision 10-Sep-1982 #text_change 09-Jul-2004
 R:Sheppard, H.W.; Gutman, G.A.
 Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981
 A:Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the leader sequence
 A:Reference number: A93901; NUID:82082587; PMID:6273908
 A:Accession: A02118
 A:Molecule type: DNA
 A:Residues: 1-106 <SHE>
 A:Cross-references: UNIPROT:P01836; GB:J02574; GB:J00745; NID:9204820; PIDN:AAA41411.1;
 A:Experimental source: strain DA
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
 C:Family: immunoglobulin C region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:19-88|Domain: Immunoglobulin homology <IMM>
 F:26-85|Disulfide bonds: #status predicted
 F:106/disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 22.2%; Score 6; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0;
 Qy 14 LSLTKV 19
 Db 71 LSLTKV 76

RESULT 13
 D72598
 hypothetical protein APE1252 - Aeropyrum pernix (strain K1)
 C-Species: Aeropyrum pernix
 C-Accession: D72598
 C-Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C:Accession: D72598
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C:Accession: D72598
 C:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix K1
 C:Reference number: A72450; NUID:9310339; PMID:10382966
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-107 <KAW>
 A:Cross-references: UNIPROT:Q9YCK5; DDBJ:AP000061; NID:95104821; PIDN:BA80242.1; PID:dn
 A:Experimental source: strain K1
 C:Keywords:
 A:Gene: APE1252

Query Match 22.2%; Score 6; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0;
 Qy 20 NATPPE 25
 Db 71 NATPPE 76

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RESULT 14
T09060
hypothetical protein NG1 - mouse
C;Species: Mus musculus (house mouse)
C;accession: T09060
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc
submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: Z16543
A;accession: T09060
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-112 <ROW>
A;Cross-references: UNIPROT:Q35443; EMBL:AF030001; NID:92564945; PID:92564948
C;Genetics:
A;Gene: NG1
A;Map position: 17
A;Introns: 13/3; 67/3

RESULT 15
H90453
hypothetical protein SSO2777 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;accession: H90453
C;date: 24-May-2001 #sequence_revision 24-May-2001 #ext_change 09-Jul-2004
C;R;She, O.; Singh, R.K.; Confalonieri, P.; Zivanovic, Y.; Allard, G.; Awazy, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Koza, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;accession: H90453
A;Status: preliminary
A;Cross-references: UNIPROT:Q97V59; GB:AE006641; NID:913816114; PIDN:AAK42887.1; GSPDB:G
A;Molecule type: DNA
A;Residues: 1-118 <KUR>
C;Genetics:
A;Gene: SSO2777

Query Match          22.2%; Score 6; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 48;
Matches   6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      7 GNLIL 12
          ||||| |
Db      21 GNLIL 26

Search completed: October 18, 2005, 13:48:10
Job time : 42 secs

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Db 14 FFAVANGNELLIDSLTKVATEPERT 40

RESULT 2 US-08-430-944D-14

Sequence 14, Application US/08430944D

Patent No. 6,025162

GENERAL INFORMATION:

APPLICANT: Bruce L. Rogers et al.

TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN

TITLE OF INVENTION:

NUMBER OF SEQUNCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSE: LARIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/430,014

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 90 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-430-014-14

Query Match 100.0%; Score 27; DB 3; Length 90;

Best Local Similarity 100.0%; Pred. No. 2.5e-19;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FFAVANGNELLIDSLTKVATEPERT 27

Db 14 FFAVANGNELLIDSLTKVATEPERT 40

RESULT 4 US-08-431-184-14

Sequence 14, Application US/08431184

Patent No. 6,120769

GENERAL INFORMATION:

APPLICANT: Bruce L. Rogers et al.

TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN

TITLE OF INVENTION:

NUMBER OF SEQUNCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSE: LARIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/431,184

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/430,014

FILING DATE: 27-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/430,014

FILING DATE: 28-APR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

RESULT 3 US-08-430-014-14

Sequence 14, Application US/08430014

Patent No. 6,08962

GENERAL INFORMATION:

APPLICANT: GERTER, Malcolm L. et al.

TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE

TITLE OF INVENTION:

NUMBER OF SEQUNCES: 101

CORRESPONDENCE ADDRESS:

ADDRESSE: IMMULOGIC PHARMACEUTICAL CORPORATION

STREET: 610 LINCOLN STREET

CITY: WALTHAM

STATE: Massachusetts

REFERENCE/DOCKET NUMBER: IMI-044DV3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEX/FAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 90 amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal

US-08-431-184-14

Query Match 100.0%; Score 27; DB 3; Length 90;

Best Local Similarity 100.0%; Pred. No. 2.5e-19; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDLSITKVNATEPERT 27
 Db 14 FFAVANGNELLIDLSITKVNATEPERT 40

RESULT 5

US-08-100-928C-13
 Sequence 13, Application US/08300928C
 Patent No. 6019972

GENERAL INFORMATION:
 APPLICANT: GEFTER, Malcolm L. et al.
 TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE PROTEIN (TRFP)

TITLE OF INVENTION: PROTEIN (TRFP)
 NUMBER OF SEQUENCES: 101
 NUMBER OF SEQUENCES: 101
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION

ADDRESSER: IMMULOGIC PHARMACEUTICAL CORPORATION
 STREET: 610 LINCOLN STREET
 CITY: WALTHAM
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02445

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENT IN RELEASE #11.0, Version #11.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/430, 944D
 FILING DATE: 20-APR-1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/300, 928
 FILING DATE: 02-SEPT-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/430, 014
 FILING DATE: 27-APR-1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 35, 207
 REGISTRATION NUMBER: 35, 207
 REFERENCE/DOCKET NUMBER: IMI-044DV2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEX/FAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 92 amino acids
 LENGTH: 92 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal

US-08-300-928C-13

REFERENCE/DOCKET NUMBER: 002-608 (IMI-044)

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
 LENGTH: 92 amino acids
 LENGTH: 92 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal

US-08-300-928C-13

Query Match 100.0%; Score 27; DB 3; Length 92;
 Best Local Similarity 100.0%; Pred. No. 2.6e-19; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDLSITKVNATEPERT 27
 Db 14 FFAVANGNELLIDLSITKVNATEPERT 40

Db 14 FFAVANGNELLIDLSITKVNATEPERT 40

RESULT 6

US-08-430-944D-13
 Sequence 13, Application US/08430944D
 Patent No. 6025162

GENERAL INFORMATION:
 APPLICANT: Bruce L. Rogers et al.
 TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
 TITLE OF INVENTION:
 NUMBER OF SEQUENCES: 103
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DAHIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PATENT IN RELEASE #11.0, Version #11.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/430, 944D
 FILING DATE: 20-APR-1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/430, 014
 FILING DATE: 27-APR-1995

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 35, 207
 REGISTRATION NUMBER: 35, 207
 REFERENCE/DOCKET NUMBER: IMI-044DV2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEX/FAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 92 amino acids
 LENGTH: 92 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal

US-08-430-944D-13

Query Match 100.0%; Score 27; DB 3; Length 92;

Best Local Similarity 100.0%; Pred. No. 2.6e-19; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLIDLSITKVNATEPERT 27
 Db 14 FFAVANGNELLIDLSITKVNATEPERT 40

RESULT 7

US-08-430-014-13

Sequence 13, Application US/08430014
 Patent No. 6043962

GENERAL INFORMATION:
 APPLICANT: GEFTER, Malcolm L. et al.
 TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE PROTEIN (TRFP)

TITLE OF INVENTION: PROTEIN (TRFP)
 NUMBER OF SEQUENCES: 101
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
 STREET: 610 LINCOLN STREET
 CITY: WALTHAM
 STATE: Massachusetts
 COUNTRY: USA

ZIP: 02145
 COMPUTER READABLE FORM:
 COMPUTER: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/430,014
 FILING DATE: 02-SEPT-1994
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/300,928
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: AMY E. MANDRAGOURAS
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 92 amino acids
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 US-08-431-184-13

Query Match 100.0%; Score 27; DB 3; Length 92;
 Best Local Similarity 100.0%; Pred. No. 2.6e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Ov 1 FFAVANGNELLIDSLSLTKVNAEPERT 27
 Db 14 FFAVANGNELLIDSLSLTKVNAEPERT 40

RESULT 8
 US-08-431-184-13
 Sequence 13, Application US/08431184
 Patent No. 6120569
 GENERAL INFORMATION:
 APPLICANT: Bruce L. Rogers et al.
 TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
 NUMBER OF SEQUENCES: 103
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LATIVE & COCKFIELD, LLP
 STREET: 28 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/300,928C
 FILING DATE: September 2, 1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/1807,529
 FILING DATE: December 13, 1991
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: AMY E. MANDRAGOURAS
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 97 amino acids
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: protein
 US-08-300-928C-10

Query Match 100.0%; Score 27; DB 3; Length 97;
 Best Local Similarity 100.0%; Pred. No. 2.7e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Ov 1 FFAVANGNELLIDSLSLTKVNAEPERT 27
 Db 33 FFAVANGNELLIDSLSLTKVNAEPERT 59

RESULT 10
 US-08-430-944D-10
 Sequence 10, Application US/08430944D
 ; Patent No. 6025162
 GENERAL INFORMATION:
 ; APPLICANT: Bruce L. Rogers et al.
 ; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
 ; NUMBER OF SEQUENCES: 103
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/430, 014
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/300, 928
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragoras
 REGISTRATION NUMBER: 36, 207
 REFERENCE/DOCKET NUMBER: 002.6US1(IMI-044)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-4400
 FAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 97 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 US-08-430-014-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 ; TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 97 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-430-944D-10
 Query Match 100.0%; Score 27; DB 3; Length 97;
 Best Local Similarity 100.0%; Pred. No. 2.7e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FFAVANGNELLIDSLSTKVNATEPERT 27
 Db 33 FFAVANGNELLIDSLSTKVNATEPERT 59
 RESULT 11
 US-08-431-184-10
 Sequence 10, Application US/08431184
 ; Patent No. 6120769
 GENERAL INFORMATION:
 ; APPLICANT: Bruce L. Rogers et al.
 ; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
 ; NUMBER OF SEQUENCES: 103
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent-in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/431, 184
 FILING DATE: 28-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/300, 928
 FILING DATE: 02-SEPT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragoras
 REGISTRATION NUMBER: 36, 207
 REFERENCE/DOCKET NUMBER: IMI-044DV2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 FAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 10:

RESULT 13
 US-07-662-193-5
 ; Sequence 5, Application US/07662193
 ; GENERAL INFORMATION:
 ; Pat. No. 53891
 ; APPLICANT: Rogers, Bruce L.
 ; TOPOLGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-431-184-10
 ; Query Match 100.0%; Score 27; DB 3; Length 97;
 ; Best Local Similarity 100.0%; Pred. No. 2.7e-19;
 ; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ;
 Qy 1 FFAVANGNELLIDSLTKVATEPERT 27
 Db 33 FFAVANGNELLIDSLTKVATEPERT 59
 ;
 RESULT 13
 US-07-662-193-5
 ; Sequence 5, Application US/07662193
 ; GENERAL INFORMATION:
 ; APPLICANT: Kuo, Mei-chang
 ; TOPOLGY: linear
 ; MOLECULE TYPE: protein
 ; TITLE OF INVENTION: Improved Preparation of Cat Dander
 ; NUMBER OF SEQUENCES: 8
 ; TITLE OF INVENTION: Allergens for Immunotherapeutic Purposes and Uses Thereof
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LATIVE & COCKFIELD
 ; STREET: 60 State Street, Suite 510
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM PC compatible
 ; COMPUTER TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII TEXT
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/807, 529A
 ; FILING DATE: 19911213
 ; CLASSIFICATION: 514
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/662, 276
 ; FILING DATE: 28-FEB-1991
 ; APPLICATION NUMBER: US 07/431, 565
 ; FILING DATE: 03-NOV-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Channing, Stacey L.
 ; REGISTRATION NUMBER: 31, 095
 ; REFERENCE/DOCKET NUMBER: IPC-027/imi-015
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 494-0060
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 109 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-807-529A-6
 ;
 ; Query Match 100.0%; Score 27; DB 1; Length 109;
 ; Best Local Similarity 100.0%; Pred. No. 3e-19;
 ; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ;
 Qy 1 FFAVANGNELLIDSLTKVATEPERT 27
 Db 33 FFAVANGNELLIDSLTKVATEPERT 59
 ;
 RESULT 14
 US-07-807-529A-6
 ; Sequence 6, Application US/07807529A
 ;
 RESULT 14
 US-07-807-529A-6
 ; Sequence 6, Application US/07807529A
 ;

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,928C
FILING DATE: September 2, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.GUS (IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-300-928C-8

Query Match 100.0%; Score 27; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FFAVANGNELLIDLSLTKVNATEGRPT 27
Db 33 FFAVANGNELLIDLSLTKVNATEGRPT 59

Search completed: October 18, 2005, 13:48:56
Job time : 43 Secs

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